5000

CRF Errors Corrected by the STIC Systems Branch

ENTERED

Serial Number: 09/868,547

CRF Processing Date: 11/6/2001
Edited by:
Verified by: _____ (STIC sta)

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically:
_____

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:
_____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
_____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
_____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included:
_____

☐ Deleted extra, invalid, headings used by an applicant, specifically:
_____

☑ Deleted: ☑ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically:
_____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically:
_____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☐ Other:
_____
_____
_____
_____

Examiner: The above corrections must be communicated to the applicant in the first Office Action! DO NOT send a copy of this form.

3/1/95

```
            RAW SEQUENCE LISTING              DATE: 11/06/2001
            PATENT APPLICATION:  US/09/868,547   TIME: 07:56:55

            Input Set : A:\PTO.AMC.txt
            Output Set: N:\CRF3\11062001\I868547.raw

       3 <110> APPLICANT: E. I. du Pont de Nemours and Company
       5 <120> TITLE OF INVENTION: Flavonoid Biosynthetic Enzymes
       7 <130> FILE REFERENCE: BB1324 1
C-->   9 <140> CURRENT APPLICATION NUMBER: US/09/868,547
C-->  10 <141> CURRENT FILING DATE: 2001-09-20
      12 <150> PRIOR APPLICATION NUMBER: 60/113,190
      13 <151> PRIOR FILING DATE: 1998-12-21
      15 <160> NUMBER OF SEQ ID NOS: 10
      17 <170> SOFTWARE: Microsoft Office 97
      19 <210> SEQ ID NO: 1
      20 <211> LENGTH: 1053
      21 <212> TYPE: DNA
      22 <213> ORGANISM: Glycine max
      24 <400> SEQUENCE: 1
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      26 gggcacctaa gacctatgtg tcttaagtgg gctgttcaac taggtattcc agacataata  120
      27 cagaaccatg ccaaacccat tacagtttct gacttggttt ctactcttca aatttcacca  180
      28 tctaaggctg gttttgtgca gcagttcatg cgctttttgg cacacgatgg aatctttgat  240
      29 atccgtgaga gccaagatga tcatgaatta gcatatgctc taacccctgc atcaaagctt  300
      30 ctagttagtt gcagtgacca ctgtttatct ccaatggttc ggatgaatac tgatccactt  360
      31 ctgatgacta cataccatca ctttggggaa tggattcgtg gggaagaccc cacagtacat  420
      32 gagacagcct tcggaacaag cttttgggga cttcttgaga aaaaccctac acaaatgagt  480
      33 ctcttcaatg aggctatggc aagtgattcc cgaatggtag acttggcact caaaaattgc  540
      34 acttcagttt ttgaagggct agattccatg gtggatgttg gtggtggaac tggaaccaca  600
      35 gccaaaatta tctgtgaggc atttccgaag ttgaaatgtg ttgtgcttga ccttcctcat  660
      36 gttgtagaaa acttgacagg aaccaataat ttgagttttg tcggtggtga tatgttcaac  720
      37 tctttccctc aaactgatgc agttctacta aagtgggttt tacataattg gaatgacgaa  780
      38 aattgcataa agatcctgaa aaagtgtaaa gattctattt caagcaaagg caacaaagga  840
      39 aaagtgatta tcatagatat aataataaat gagaagctag atgatccgga tatgactcga  900
      40 acaaagctta gtttggatat agttatgtcg actatgaatg gaagagagcg aagtgaaaaa  960
      41 gaatggaaac aaatgttcat tgaagcggga ttcaaacact gcaaaatatt tcccatcttt 1020
      42 ggtttcagat ctctaattga gctctatcct tag                               1053
      44 <210> SEQ ID NO: 2
      45 <211> LENGTH: 350
      46 <212> TYPE: PRT
      47 <213> ORGANISM: Glycine max
      49 <400> SEQUENCE: 2
      50 Asp Asn Gln Lys Ala Met Glu Leu Phe Glu Gly Gln Ser Leu Leu Tyr
      51  1               5                  10                  15
      53 Met Gln Leu Tyr Gly His Leu Arg Pro Met Cys Leu Lys Trp Ala Val
      54              20                  25                  30
      56 Gln Leu Gly Ile Pro Asp Ile Ile Gln Asn His Ala Lys Pro Ile Thr
      57          35                  40                  45
      59 Val Ser Asp Leu Val Ser Thr Leu Gln Ile Ser Pro Ser Lys Ala Gly
      60      50                  55                  60
      62 Phe Val Gln Gln Phe Met Arg Phe Leu Ala His Asp Gly Ile Phe Asp
      63  65                  70                  75                  80
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RAW SEQUENCE LISTING   DATE: 11/06/2001
PATENT APPLICATION: US/09/868,547   TIME: 07:56:55

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\11062001\I868547.raw

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 65 Ile Arg Glu Ser Gln Asp Asp His Glu Leu Ala Tyr Ala Leu Thr Pro
 66               85                  90                  95
 68 Ala Ser Lys Leu Leu Val Ser Cys Ser Asp His Cys Leu Ser Pro Met
 69             100                 105                 110
 71 Val Arg Met Asn Thr Asp Pro Leu Leu Met Thr Thr Tyr His His Phe
 72             115                 120                 125
 74 Gly Glu Trp Ile Arg Gly Glu Asp Pro Thr Val His Glu Thr Ala Phe
 75     130                 135                 140
 77 Gly Thr Ser Phe Trp Gly Leu Leu Glu Lys Asn Pro Thr Gln Met Ser
 78 145                 150                 155                 160
 80 Leu Phe Asn Glu Ala Met Ala Ser Asp Ser Arg Met Val Asp Leu Ala
 81             165                 170                 175
 83 Leu Lys Asn Cys Thr Ser Val Phe Glu Gly Leu Asp Ser Met Val Asp
 84             180                 185                 190
 86 Val Gly Gly Gly Thr Gly Thr Thr Ala Lys Ile Ile Cys Glu Ala Phe
 87             195                 200                 205
 89 Pro Lys Leu Lys Cys Val Val Leu Asp Leu Pro His Val Val Glu Asn
 90     210                 215                 220
 92 Leu Thr Gly Thr Asn Asn Leu Ser Phe Val Gly Gly Asp Met Phe Asn
 93 225                 230                 235                 240
 95 Ser Phe Pro Gln Thr Asp Ala Val Leu Leu Lys Trp Val Leu His Asn
 96             245                 250                 255
 98 Trp Asn Asp Glu Asn Cys Ile Lys Ile Leu Lys Lys Cys Lys Asp Ser
 99             260                 265                 270
101 Ile Ser Ser Lys Gly Asn Lys Gly Lys Val Ile Ile Ile Asp Ile Ile
102         275                 280                 285
104 Ile Asn Glu Lys Leu Asp Asp Pro Asp Met Thr Arg Thr Lys Leu Ser
105     290                 295                 300
107 Leu Asp Ile Val Met Ser Thr Met Asn Gly Arg Glu Arg Ser Glu Lys
108 305                 310                 315                 320
110 Glu Trp Lys Gln Met Phe Ile Glu Ala Gly Phe Lys His Cys Lys Ile
111                 325                 330                 335
113 Phe Pro Ile Phe Gly Phe Arg Ser Leu Ile Glu Leu Tyr Pro
114             340                 345                 350
116 <210> SEQ ID NO: 3
117 <211> LENGTH: 1160
118 <212> TYPE: DNA
119 <213> ORGANISM: Glycine max
121 <400> SEQUENCE: 3
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123 tcaagctctc ttgtacaaac atttgcttgg cttcatagat tctaagtgtc taaaatggat  120
124 ggttgagctt gacatacccg acataatcca cagccatagc catggccaac ccattacttt  180
125 ttcagagttg gtgtcaattc tacaagtccc accaactaaa actcgtcagg tgcagagcct  240
126 catgcgttat ctagcacaca atggattctt tgagatagta agaatccatg acaacataga  300
127 agcatatgct ctcactgctg cttcagagtt acttgtcaaa agcagtgagc ttagtttagc  360
128 tccaatggtt gagtattttc ttgaaccaaa ttgtcaaggt gcatggaacc agttgaagag  420
129 gtgggttcat gaggaagatc tcacagtatt tgaggtctcc ttaggaacac ctttctggga  480
130 ctttatcaat aaagaccctg catataacaa gtcattcaat gaggcaatgg cttgtgattc  540
131 tcagatgttg aacttggcgt ttagagattg caattgggtc tttgagggac tggaatccat  600
```

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132 tgtggatgtt ggtggtggaa ctggaatcac agcaaagatt atctgtgagg cttttcctaa  660
133 gctgaaatgc atggtgttgg aacgtccaaa tgttgtggaa aatttgtcag gaagcaacaa  720
134 tttgacattt gttggtgggg acatgtttaa atgcatcccc aaggctgatg cagttctgct  780
135 taagttggtt ttacataatt ggaatgacaa cgattgcatg aagatattag aaaattgtaa  840
136 agaagctatt tcaggtgaaa gcaaaacagg aaaagtagtt gtcatagata ctgtgataaa  900
137 cgaaaacaaa gatgagcgcc aagttactga actaaagctc cttatggatg tacacatggc  960
138 atgtattatt aatggaaaag agagaaaaga agaagattgg aagaaactct tcatggaagc 1020
139 agggttccaa agctacaaaa tatctccctt cacaggatat ttgtctctta ttgagatcta 1080
140 tccttgaata ctgacgctgc aatattccat ttagtagtta atttgcatgt tatcaataaa 1140
141 ataaaagtta tctttgtgtt                                              1160
143 <210> SEQ ID NO: 4
144 <211> LENGTH: 358
145 <212> TYPE: PRT
146 <213> ORGANISM: Glycine max
148 <400> SEQUENCE: 4
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150  1               5                   10                  15
152 Gly Gln Ala Leu Leu Tyr Lys His Leu Leu Gly Phe Ile Asp Ser Lys
153              20                  25                  30
155 Cys Leu Lys Trp Met Val Glu Leu Asp Ile Pro Asp Ile Ile His Ser
156          35                  40                  45
158 His Ser His Gly Gln Pro Ile Thr Phe Ser Glu Leu Val Ser Ile Leu
159      50                  55                  60
161 Gln Val Pro Pro Thr Lys Thr Arg Gln Val Gln Ser Leu Met Arg Tyr
162  65                  70                  75                  80
164 Leu Ala His Asn Gly Phe Phe Glu Ile Val Arg Ile His Asp Asn Ile
165              85                  90                  95
167 Glu Ala Tyr Ala Leu Thr Ala Ala Ser Glu Leu Leu Val Lys Ser Ser
168              100                 105                 110
170 Glu Leu Ser Leu Ala Pro Met Val Glu Tyr Phe Leu Glu Pro Asn Cys
171          115                 120                 125
173 Gln Gly Ala Trp Asn Gln Leu Lys Arg Trp Val His Glu Glu Asp Leu
174      130                 135                 140
176 Thr Val Phe Glu Val Ser Leu Gly Thr Pro Phe Trp Asp Phe Ile Asn
177 145                 150                 155                 160
179 Lys Asp Pro Ala Tyr Asn Lys Ser Phe Asn Glu Ala Met Ala Cys Asp
180              165                 170                 175
182 Ser Gln Met Leu Asn Leu Ala Phe Arg Asp Cys Asn Trp Val Phe Glu
183              180                 185                 190
185 Gly Leu Glu Ser Ile Val Asp Val Gly Gly Gly Thr Gly Ile Thr Ala
186          195                 200                 205
188 Lys Ile Ile Cys Glu Ala Phe Pro Lys Leu Lys Cys Met Val Leu Glu
189      210                 215                 220
191 Arg Pro Asn Val Val Glu Asn Leu Ser Gly Ser Asn Asn Leu Thr Phe
192 225                 230                 235                 240
194 Val Gly Gly Asp Met Phe Lys Cys Ile Pro Lys Ala Asp Ala Val Leu
195              245                 250                 255
197 Leu Lys Leu Val Leu His Asn Trp Asn Asp Asn Asp Cys Met Lys Ile
198          260                 265                 270
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RAW SEQUENCE LISTING   DATE: 11/06/2001
PATENT APPLICATION: US/09/868,547   TIME: 07:56:55

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\11062001\I868547.raw

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200 Leu Glu Asn Cys Lys Glu Ala Ile Ser Gly Glu Ser Lys Thr Gly Lys
201         275             280             285
203 Val Val Val Ile Asp Thr Val Ile Asn Glu Asn Lys Asp Glu Arg Gln
204         290             295             300
206 Val Thr Glu Leu Lys Leu Leu Met Asp Val His Met Ala Cys Ile Ile
207 305             310             315             320
209 Asn Gly Lys Glu Arg Lys Glu Glu Asp Trp Lys Lys Leu Phe Met Glu
210             325             330             335
212 Ala Gly Phe Gln Ser Tyr Lys Ile Ser Pro Phe Thr Gly Tyr Leu Ser
213         340             345             350
215 Leu Ile Glu Ile Tyr Pro
216         355
218 <210> SEQ ID NO: 5
219 <211> LENGTH: 1065
220 <212> TYPE: DNA
221 <213> ORGANISM: Glycine max
223 <400> SEQUENCE: 5
224 atggcttcaa tgaataacca aaaagaaatt gagctctttg agggccaatc tcttctgtac   60
225 atgcagctat atgggcacct aagacctatg tgtcttaagt gggctgttca actaggtatt  120
226 ccagacataa tacagaacca tgccaaaccc atttctcttt ctgacttggt ctctactctt  180
227 caaattccac cagctaacgc tgcttttgtg cagcggttca tgcgcttctt ggcacacaat  240
228 ggaatctttg agatccatga gagccaagaa gatcatgaac taacatatgc tctaccccct  300
229 gcatcaaagc ttcttgtcaa tagtagtgat cattgtctat ctccaatggt tctagcgttt  360
230 accgatccac ttcggaacgt taaataccat cacttggggg aatggattcg tggggaggac  420
231 ccctcagtat ttgagacagc ccacggaaca agcgcttggg gacttcttga gaaaaatcct  480
232 gaatatttta gtctcttcaa tgaggctatg gcaagtgatt cccgaatagt agacttggca  540
233 ctcaaaaatt gcacttcagt ttttgagggg ctagattcca tggtggatgt tggtggtgga  600
234 actggaacca cggccagaat tatctgtgac gcatttccta agttgaaatg tgttgtgctt  660
235 gaccttcctc atgttgtaga gaacttgaca gggaccaata atttgagttt tgttggtggt  720
236 gacatgttca actctatccc tcaagctgat gcagtgctac taaagtgggt tttacataat  780
237 tggaccgacg aaaattgcat aaagatcctg caaaagtgta gagattctat ttcaagcaaa  840
238 ggcaacagtg gaaaagtgat tatcatagat gccgtaataa atgagaagct agatgacccg  900
239 gatatgacac aaacaaagct tagtttggac attattatgt tgacgatgaa tggaagagag  960
240 agaacggaaa agaatggaa  acaactcttc atcgaagcag gattcaaaca ctacaaaata 1020
241 tttcccatct ttggttttag atctctgatt gaggtctatc cttga               1065
243 <210> SEQ ID NO: 6
244 <211> LENGTH: 351
245 <212> TYPE: PRT
246 <213> ORGANISM: Glycine max
248 <400> SEQUENCE: 6
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250   1             5             10             15
252 Ser Leu Leu Tyr Met Gln Leu Tyr Gly His Leu Arg Pro Met Cys Leu
253         20             25             30
255 Lys Trp Ala Val Gln Leu Gly Ile Pro Asp Ile Ile Gln Asn His Ala
256         35             40             45
258 Lys Pro Ile Ser Leu Ser Asp Leu Val Ser Thr Leu Gln Ile Pro Pro
259       50             55             60
261 Ala Asn Ala Ala Phe Val Gln Arg Phe Met Arg Phe Leu Ala His Asn
```

```
262  65                        70                      75                        80
264  Gly Ile Phe Glu Ile His Glu Ser Gln Glu Leu Thr Tyr Ala Leu Thr
265                  85                      90                      95
267  Pro Ala Ser Lys Leu Leu Val Asn Ser Ser Asp His Cys Leu Ser Pro
268                 100                     105                     110
270  Met Val Leu Ala Phe Thr Asp Pro Leu Arg Asn Val Lys Tyr His His
271             115                     120                     125
273  Leu Gly Glu Trp Ile Arg Gly Glu Asp Pro Ser Val Phe Glu Thr Ala
274         130                     135                     140
276  His Gly Thr Ser Ala Trp Gly Leu Leu Glu Lys Asn Pro Glu Tyr Phe
277  145                     150                     155                     160
279  Ser Leu Phe Asn Glu Ala Met Ala Ser Asp Ser Arg Ile Val Asp Leu
280                 165                     170                     175
282  Ala Leu Lys Asn Cys Thr Ser Val Phe Glu Gly Leu Asp Ser Met Val
283                 180                     185                     190
285  Asp Val Gly Gly Gly Thr Gly Thr Thr Ala Arg Ile Ile Cys Asp Ala
286             195                     200                     205
288  Phe Pro Lys Leu Lys Cys Val Val Leu Asp Leu Pro His Val Val Glu
289         210                     215                     220
291  Asn Leu Thr Gly Thr Asn Asn Leu Ser Phe Val Gly Gly Asp Met Phe
292  225                     230                     235                     240
294  Asn Ser Ile Pro Gln Ala Asp Ala Val Leu Leu Lys Trp Val Leu His
295                 245                     250                     255
297  Asn Trp Thr Asp Glu Asn Cys Ile Lys Ile Leu Gln Lys Cys Arg Asp
298             260                     265                     270
300  Ser Ile Ser Ser Lys Gly Asn Ser Gly Lys Val Ile Ile Ile Asp Ala
301             275                     280                     285
303  Val Ile Asn Glu Lys Leu Asp Asp Pro Asp Met Thr Gln Thr Lys Leu
304         290                     295                     300
306  Ser Leu Asp Ile Ile Met Leu Thr Met Asn Gly Arg Glu Arg Thr Glu
307  305                     310                     315                     320
309  Lys Glu Trp Lys Gln Leu Phe Ile Glu Ala Gly Phe Lys His Tyr Lys
310                 325                     330                     335
312  Ile Phe Pro Ile Phe Gly Phe Arg Ser Leu Ile Glu Val Tyr Pro
313             340                     345                     350
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316  <211> LENGTH: 1253
317  <212> TYPE: DNA
318  <213> ORGANISM: Glycine max
320  <400> SEQUENCE: 7
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322  cctaagacct atgtgtctta agtgggctgt tcaactaggt attccagaca taatacagaa   120
323  ccatgccaaa cccattactc tttctgattt ggtctctact cttcaaattc caccatctaa   180
324  ggctggtttt gtgcagcagt tcatgcgctt tttggcacac gatggaatct ttgatatccg   240
325  tgagagccaa gatgatcatg aattagcata tgctctaacc cctgcttcaa agcttctagt   300
326  tagttgcagt gaccactgtt tatctccaat ggttcggatg aatactgatc cacttctgat   360
327  gactacatac catcactttg gggaatggat tcgtggggaa gaccccacag tacatgagac   420
328  agccttcgga acaagctttt ggggacttct tgagaaaaac cctacacaaa tgagtctctt   480
329  caatgaggct atggcaagtg attcccgaat ggtagacttg gcactcaaaa attgcacttc   540
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VERIFICATION SUMMARY   DATE: 11/06/2001
PATENT APPLICATION: US/09/868,547   TIME: 07:56:56

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\11062001\I868547.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

PCT09

RAW SEQUENCE LISTING   DATE: 10/30/2001
PATENT APPLICATION: US/09/868,547   TIME: 14:05:44

Input Set : A:\BB1324 PCT 01 Seq List.txt
Output Set: N:\CRF3\10302001\I868547.raw

Does Not Comply
Corrected Diskette Needed

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       3 <110> APPLICANT: E. I. du Pont de Nemours and Company
       5 <120> TITLE OF INVENTION: Flavonoid Biosynthetic Enzymes
       7 <130> FILE REFERENCE: BB1324 1
C-->   9 <140> CURRENT APPLICATION NUMBER: US/09/868,547
C-->  10 <141> CURRENT FILING DATE: 2001-09-20
      12 <150> PRIOR APPLICATION NUMBER: 60/113,190
      13 <151> PRIOR FILING DATE: 1998-12-21
      15 <160> NUMBER OF SEQ ID NOS: 10
      17 <170> SOFTWARE: Microsoft Office 97
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ERRORED SEQUENCES

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     440 <210> SEQ ID NO: 10
     441 <211> LENGTH: 350
     442 <212> TYPE: PRT
     443 <213> ORGANISM: Glycine max
     445 <400> SEQUENCE: 10
     446 Ala Ser Met Asn Asn Gln Lys Glu Ile Glu Leu Phe Glu Gly Gln Ser
     447  1               5                   10                  15
     449 Leu Leu Tyr Met Gln Leu Tyr Gly His Leu Arg Pro Met Cys Leu Lys
     450              20                  25                  30
     452 Trp Ala Val Gln Leu Gly Ile Pro Asp Ile Ile Gln Asn His Ala Lys
     453          35                  40                  45
     455 Pro Ile Ser Leu Ser Asp Leu Val Ser Thr Leu Gln Ile Pro Pro Ala
     456      50                  55                  60
     458 Asn Ala Ala Phe Val Gln Arg Phe Met Arg Phe Leu Ala His Asn Gly
     459 65                  70                  75                  80
     461 Ile Phe Glu Ile His Glu Ser Gln Glu Leu Thr Tyr Ala Leu Thr Pro
     462              85                  90                  95
     464 Ala Ser Lys Leu Leu Val Asn Ser Ser Asp His Cys Leu Ser Pro Met
     465             100                 105                 110
     467 Val Leu Ala Phe Thr Asp Pro Leu Arg Asn Val Lys Tyr His His Leu
     468             115                 120                 125
     470 Gly Glu Trp Ile Arg Gly Glu Asp Pro Ser Val Phe Glu Thr Ala His
     471         130                 135                 140
     473 Gly Thr Ser Ala Trp Gly Leu Leu Glu Lys Asn Pro Glu Tyr Phe Ser
     474 145                 150                 155                 160
     476 Leu Phe Asn Glu Ala Met Ala Ser Asp Ser Arg Ile Val Asp Leu Ala
     477             165                 170                 175
     480 Leu Lys Asn Cys Thr Ser Val Phe Glu Gly Leu Asp Ser Met Val Asp
     481             180                 185                 190
     483 Val Gly Gly Gly Thr Gly Thr Thr Ala Arg Ile Ile Cys Asp Ala Phe
     484             195                 200                 205
     486 Pro Lys Leu Lys Cys Val Val Leu Asp Leu Pro His Val Val Glu Asn
     487         210                 215                 220
     489 Leu Thr Gly Thr Asn Asn Leu Ser Phe Val Gly Gly Asp Met Phe Asn
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RAW SEQUENCE LISTING   DATE: 10/30/2001
PATENT APPLICATION: US/09/868,547   TIME: 14:05:44

Input Set : A:\BB1324 PCT 01 Seq List.txt
Output Set: N:\CRF3\10302001\I868547.raw

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490 225
492 Ser Ile Pro Gln Ala Asp Ala Val Leu Leu Lys Trp Val Leu His Asn
493                 245                 250                 255
495 Trp Thr Asp Glu Asn Cys Ile Lys Ile Leu Gln Lys Cys Arg Asp Ser
496                 260                 265                 270
498 Ile Ser Ser Lys Gly Asn Ser Gly Lys Val Ile Ile Ile Asp Ala Val
499             275                 280                 285
501 Ile Asn Glu Lys Leu Asp Asp Pro Asp Met Thr Gln Thr Lys Leu Ser
502         290                 295                 300
504 Leu Asp Ile Ile Met Leu Thr Met Asn Gly Arg Glu Arg Thr Glu Lys
505 305                 310                 315                 320
507 Glu Trp Lys Gln Leu Phe Ile Glu Ala Gly Phe Lys His Tyr Lys Ile
508                 325                 330                 335
510 Phe Pro Ile Phe Gly Phe Arg Ser Leu Ile Glu Val Tyr Pro
511                 340                 345                 350
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E--> 513 (9)

VERIFICATION SUMMARY DATE: 10/30/2001
PATENT APPLICATION: US/09/868,547 TIME: 14:05:45

Input Set : A:\BB1324 PCT 01 Seq List.txt
Output Set: N:\CRF3\10302001\I868547.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:513 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10